Lin Lin

List of Publications by Year
in descending order

16 papers	619 citations	840776	996975
		11 h-index	15 g-index

16 all docs	16 docs citations	16 times ranked	1075 citing authors

#	Article	IF	Citations
1	LC-MS based serum metabonomic analysis for renal cell carcinoma diagnosis, staging, and biomarker discovery. Journal of Proteome Research, 2011, 10, 1396-1405.	3.7	135
2	Direct infusion mass spectrometry or liquid chromatography mass spectrometry for human metabonomics? A serum metabonomic study of kidney cancer. Analyst, The, 2010, 135, 2970.	3.5	133
3	<scp>LC</scp>â€‹<scp>MS</scp>â€‹based serum metabolic profiling for genitourinary cancer classification and cancer typeâ€‹specific biomarker discovery. Proteomics, 2012, 12, 2238-2246.	2.2	67
4	High throughput and accurate serum proteome profiling by integrated sample preparation technology and single-run data independent mass spectrometry analysis. Journal of Proteomics, 2018, 174, 9-16.	2.4	66
5	Identification, Quantification, and Site Localization of Protein Posttranslational Modifications via Mass Spectrometry-Based Proteomics. Advances in Experimental Medicine and Biology, 2016, 919, 345-382.	1.6	51
6	Spatial-Resolution Cell Type Proteome Profiling of Cancer Tissue by Fully Integrated Proteomics Technology. Analytical Chemistry, 2018, 90, 5879-5886.	6.5	35
7	Mixed-mode ion exchange-based integrated proteomics technology for fast and deep plasma proteome profiling. Journal of Chromatography A, 2018, 1564, 76-84.	3.7	28
8	3D-SISPROT: A simple and integrated spintip-based protein digestion and three-dimensional peptide fractionation technology for deep proteome profiling. Journal of Chromatography A, 2017, 1498, 207-214.	3.7	26
9	Holistic metabonomic profiling of urine affords potential early diagnosis for bladder and kidney cancers. Metabolomics, 2013, 9, 119-129.	3.0	23
10	Fast quantitative urinary proteomic profiling workflow for biomarker discovery in kidney cancer. Clinical Proteomics, 2018, 15, 42.	2.1	16
11	Advancing serum peptidomic profiling by data-independent acquisition for clear-cell renal cell carcinoma detection and biomarker discovery. Journal of Proteomics, 2020, 215, 103671.	2.4	15
12	Peptidome workflow of serum and urine samples for biomarker discovery. Analytical Methods, 2011, 3, 773.	2.7	11
13	Application of a Pseudotargeted MS Method for the Quantification of Glycated Hemoglobin for the Improved Diagnosis of Diabetes Mellitus. Analytical Chemistry, 2020, 92, 3237-3245.	6.5	8
14	SH2 Domains as Affinity Reagents for Phosphotyrosine Protein Enrichment and Proteomic Analysis. Methods in Molecular Biology, 2017, 1555, 395-406.	0.9	3
15	A Comparative Study of Elution Gradients in UPLC-TOF-MS-Based Metabonomics Research. Chromatographia, 2010, 72, 807-813.	1.3	2
16	Improved profiling of low molecular weight serum proteome for gastric carcinoma by data-independent acquisition. Analytical and Bioanalytical Chemistry, 0, , .	3.7	0